

#9



OIPE

## ENTERED

## RAW SEQUENCE LISTING

DATE: 03/18/2002

PATENT APPLICATION: US/09/805,694B

TIME: 14:50:15

Input Set : A:\REVISED CORRECTED SEQUENCE LISTING BB-1432.txt  
Output Set: N:\CRF3\03182002\I805694B.raw

3 <110> APPLICANT: Kinney, Anthony  
5 <120> TITLE OF INVENTION: Hypoallergenic Transgenic Soybeans  
7 <130> FILE REFERENCE: BB1432 US NA  
9 <140> CURRENT APPLICATION NUMBER: US/09/805,694B  
10 <141> CURRENT FILING DATE: 2001-03-14  
12 <150> PRIOR APPLICATION NUMBER: 60/189,823  
13 <151> PRIOR FILING DATE: 2000-03-16  
15 <160> NUMBER OF SEQ ID NOS: 16  
17 <170> SOFTWARE: Microsoft Office 97  
19 <210> SEQ ID NO: 1  
20 <211> LENGTH: 1156  
21 <212> TYPE: DNA  
22 <213> ORGANISM: chimeric construct  
24 <400> SEQUENCE: 1  
25 gcggccgcat gggtttccctt gtgttgcttc ttttctccctt cttaggtctc ttttttagtt 60  
26 ccagcatatc aactcatcggt tccatattgg accttgcacctt accaaaggttt accacacaga 120  
27 aacagggtgtc ttcaactgttc caactatggg agagtggca tggacgtgtc taccataacc 180  
28 acgaagaaga ggcaaagaga ctggagattt tcaagaataa ctcgaactat atcaggggaca 240  
29 tgaatgc当地 cagaaaatca cccattctc atcggtttagg attgaacaag tttgtgaca 300  
30 tcactcctca agagttcagc aaaaagtaact tgcaagctcc caaggatgtg tcgc当地aaa 360  
31 tcaaaaatggc caacaagaaa atgaagaagg aacaatattt ttgtgaccat ccacctgtcat 420  
32 catgggattt gaggaaaaaa ggtgtcatca cccaaataaa gtaccaagggg ggctgtggaa 480  
33 ggggttggc gtttttgc当地 acgggagccaa tagaagcagc acatgcaata gcaacaggag 540  
34 acottgttag ctttttgc当地 caagaactcg tagactgtgt ggaagaaaagc gaaggttt 600  
35 acaatggatg gcaatgtatcaa tcgttgc当地 gggttttaga acatgggtgc attgccactg 660  
36 atgatgatta tccttacaga gctaaagagg gtagatgcaaa agccaataaag atacaagaca 720  
37 aggttacaat tgacggatataat gaaactctaa taatgtcaga tgagagtaca gaatcagaga 780  
38 cagagcaago gttcttaagc gccatcctt agcaaccaat tagtgc当地 attgatgcaaa 840  
39 aagattttca tttatacacc gggggaaattt atgatggaga aaactgtaca agtccgtatg 900  
40 ggattaatca ctttgttta ctgtgggtt atggttcagc ggatgggtta gattactgg 960  
41 tagcgaaaaaa ttcatgggaa gaagattggg gagaagatgg ttacatttttgg atccaaagaa 1020  
42 acacgggtaa tttatttagga gtgtgtgggaa tgaatttattt cgcttc当地 ccaaccaaag 1080  
43 aggaatcaga aacactgggt tctgctcgcc ttaaaggta tcgaagagtt gatcactctc 1140  
44 ctcttgagc ggccgc 1156  
46 <210> SEQ ID NO: 2  
47 <211> LENGTH: 2970  
48 <212> TYPE: DNA  
49 <213> ORGANISM: chimeric construct  
51 <400> SEQUENCE: 2  
52 aagcttgc当地 catggcccttc atttgc当地 attaattttt ttggtaacag tagtccgtac 60  
53 taatcagttt cttatcctt cttccatcata attaatctt gtagtctc当地 atgc当地aaac 120  
54 actgactgtt ctcttgatgc当地 ataagaaaaaa gccaagggaaac aaaagaagac aaaacacaat 180  
55 gagagtatcc ttgc当地atgc当地 aatgtctaag ttccataaaat tcaaacaaaaa acgcaatcac 240

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56	acacagtgg	catcacttat	ccactagctg	aatcaggatc	gccgcgtcaa	aaaaaaaaaa	300
57	ctggacccc	aaagccatgc	acaacaacac	gtactcacaa	aggtgtcaat	cgagcagccc	360
58	aaaacattca	ccaactcaac	coatcatgag	ccctcacatt	tgttgttct	aaccacaccc	420
59	caaactcgta	ttctctccg	ccacccatt	tttgtttatt	tcaacacccg	tcaaactgca	480
60	tgccaccccg	tggccaaatg	tccatgcatg	ttaacaagac	ctatgactat	aaatatctgc	540
61	aatctcgcc	caggtttca	tcatcaagaa	ccagttcaat	atccttagtac	accgtattaa	600
62	agaatttaag	ataactaac	agcggccgca	tgggttcct	tgtgttgctt	ctttctccc	660
63	tcttaggtct	ctcttctagt	tccagcatat	caactcatcg	ttccatatattg	gaccttgacc	720
64	taaccaagtt	taccacacag	aaacaggtgt	cttcaactgtt	ccaactatgg	aagagtgagc	780
65	atggacgtgt	ctaccataac	cacgaagaag	aggcaaaagag	acttgagatt	ttcaagaata	840
66	actcgaacta	tatcaggggac	atgaatgcaa	acagaaaatc	accccattct	catcgtttag	900
67	gattgaacaa	gtttgtgtac	atcactcctc	aagaggtcag	aaaaaaagtac	ttgcaagctc	960
68	ccaaggatgt	gtcgcagcaa	atcaaaaatgg	ccaacaagaa	aatgaagaag	gaacaatatt	1020
69	cttgcacca	tccacccgtca	tcatgggatt	ggagggaaaaa	aggtgtcatc	acccaaatgaa	1080
70	agtaccaagg	gggctgtgg	aggggttggg	cgtttctgc	cacggggagcc	atagaagcag	1140
71	cacatgcaat	agcaacagga	gaccttgtta	gccttctga	acaagaactc	gtagactgtg	1200
72	tggaaagaaag	cgaaggttct	tacaatggat	ggcagttatca	atcgttcgaa	tgggttttag	1260
73	aacatggtgg	cattgcact	gatgatgatt	atccttacag	agctaaagag	ggttagatgca	1320
74	aagccaataa	gataacaagac	aaggtttacaa	ttgacggata	tgaaaactcta	ataatgtcag	1380
75	atgagagttac	agaatcagag	acagagcaag	cgttcttaag	cgccttcctt	gagcaaccaa	1440
76	ttagtgtctc	aattgtatgca	aaagattttc	atttatacac	cggggaaatt	tatgtatggag	1500
77	aaaactgtac	aagtccgtat	gggatataatc	actttttttt	acttgcgtt	tatgtttcag	1560
78	cgatgggtt	agattactgg	atagcgaaaaa	attcatgggg	agaagattgg	ggagaagatg	1620
79	gttacatttg	gatccaaaga	aacacgggta	atttatttagg	agtgtgtgg	atgaattatt	1680
80	tcgttcata	ccccacccaa	gaggaatcag	aaacactgg	gtctgctcgc	gttaaaggc	1740
81	atcgaagagt	tgtacactc	cctcttgcgt	cggccctac	atggccacgt	gcatgaagta	1800
82	tgaactaaaa	tgcatgttag	tgtaaagagct	catggagagc	atgaaatatt	gtatccgacc	1860
83	atgttaacagt	ataataactg	agctccatct	cacttcttct	atgaaataaac	aaaggatgtt	1920
84	atgatataatt	aacactctat	ctatgcaccc	tattttcta	tgataaaattt	cctcttatta	1980
85	ttataaaatca	tctgaatcgt	gacggcttat	ggaatgcttc	aaatagtaca	aaaacaaatg	2040
86	tgtactataa	gacttctaa	acaattctaa	cttttagcatt	gtgaacgaga	cataagtgtt	2100
87	aagaagacat	aacaattata	atggaagaag	tttgctcca	tttatatatt	atatattacc	2160
88	cacttatgt	ttatatttagg	atgttaagga	gacataacaa	ttataaagag	agaagttgt	2220
89	atccatttat	atattatata	ctacccattt	atattatata	cttacccact	tatttaatgt	2280
90	cttataaagg	tttgatccat	gatatttcta	atattttatg	tgtatatgtat	atgaaagggt	2340
91	actatttggaa	ctctcttact	ctgtataaaag	gttggatcat	ccttaaagtg	ggtcttattt	2400
92	attttatttgc	ttcttacaga	taaaaaaaaattat	ggtttgataa	aatatttgcag	2460	
93	gatttaaaat	aataataaaat	aataaataaac	atataatata	tgtatataaa	tttatttataa	2520
94	tataacattt	atctataaaa	aagtaaaatat	tgtcataaaat	ctatacaatc	gtttagcctt	2580
95	gctggacgac	totcaattat	ttaaacgaga	gtaaacatata	ttgacttttt	ggttattttaa	2640
96	caaatttata	tttaacacta	tatgaaattt	tttttttta	ttagcaaaga	aataaaatta	2700
97	aattaagaag	gacaatgggt	tgtcccaatc	cttatacaac	caactccac	aagaaagtca	2760
98	agtcagagac	aacaaaaaaa	caagcaaagg	aaattttta	atttgagttt	tcttgc	2820
99	tgcataattt	atgcagtaaa	acactacaca	taaccctttt	agcagtagag	caatgggtga	2880
100	ccgtgtgctt	agcttctttt	attttatttt	tttacagca	aagaataaaat	aaaataaaat	2940
101	gagacacttc	agggatgttt	caacaagctt				2970
103	<210>	SEQ ID NO:	3				
104	<211>	LENGTH:	1600				
105	<212>	TYPE:	DNA				

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106 <213> ORGANISM: Glycine max  
 108 <400> SEQUENCE: 3  
 109 gggaaacaa aactaccctt ttgctttgc tctttgtct ttgtcatgga gtggccacaa 60  
 110 caacaatggc cttccgtat gatgagggtg gtataaaaaa gtcaccaaaa agtttgttt 120  
 111 ttagtgcacaa ctccacgagg gtttcaaga ctgcattcagg gaaatgcgt gtgtgaaaa 180  
 112 gccatggtg taggatattt tataggcaca tcgcattgg cttcatctt atgaaaccaa 240  
 113 agtccttgtt tgccctcag tacctcgact ccaatctcat catattcatc cgtagagggg 300  
 114 aagcaaagct gggattcata tatgtatgt aactagcga aaggagattt aagacagggg 360  
 115 acttgtacat gattccatct gttcagcat tctatttggt gaacatagga gaaggtcaga 420  
 116 gacttcacgt tatctgcagc attgaccctt ctacaagctt gggatttagag accttccagt 480  
 117 cttctatat tggggagga gccaattcgc actcgtgtt ttctggattt gAACCTGCCA 540  
 118 tccttggaaac tgcatttaat gaatcaagaa cgggtgtt gAAATCTTC TCCAAGGAAC 600  
 119 tagatgggcc aattatgttc gtggatgatt ctatgcacc tagcttatgg actaaattcc 660  
 120 ttcaactgaa gaaggatgac aaagagcaac agctgaagaa aatgtatgca gaccaagagg 720  
 121 aggtgagga ggagaagcaa acaagtaggt catggaggaa gctctggaa accgtattt 780  
 122 ggaagggtgaa tgagaagata gagaacaaag acactgctgg ttcccctgcc tcttacaacc 840  
 123 tctacgatga caaaaaagcc gatttcaaaa acgcttatgg ttggagcaag gcaactgcatt 900  
 124 gaggcggatca tcctccactc agcgaacccg atattggat tttacttgc aaactctcag 960  
 125 cgggatccat gttggcacct catgtgaatc caatatcaga tgagtatacc atagtgtga 1020  
 126 gtggttatgg tgaactgcattt atagggtatc caaacggaa gaaagcaatg aaaactaaaa 1080  
 127 tcaaacaagg ggacgtgtt gttgtgccaa gatacttccc cttctgtcaa gtagcatcaa 1140  
 128 gggatggacc ctttagagtcc ttggcttcc ccacttctgc aaggaagaac aagccacagt 1200  
 129 ttctggctgg tgctgcgtcc cttctaagga ctttgatggg gcccggagctt tcggccggcgt 1260  
 130 tcggagtgag cgaggacacg ttgcggcgcg ctgttgcattc tcagcatgag gctgtgatac 1320  
 131 tgccatcagc atggctgca ccacccggaaa atgcaggaa gctgaagatg gaagaagagc 1380  
 132 caaatgctat tagaagcttt gccaatgtatg tggatggaa tggatggaa tttgaacact 1440  
 133 tgattttggaa taggggttat ttggatgtc tagtgcctag tggatggaa tggatggaa 1500  
 134 ttgttctttt atatttagtt gagatgtgtt ttgttctt gagatgtgaa taatataatcta 1560  
 135 ctttctttgt gcarraaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 1600  
 137 <210> SEQ ID NO: 4  
 138 <211> LENGTH: 454  
 139 <212> TYPE: PRT  
 140 <213> ORGANISM: Glycine max  
 142 <400> SEQUENCE: 4  
 143 Met ala Phe Arg Asp Asp Glu Gly Gly Asp Lys Lys Ser Pro Lys Ser  
 144 1 5 10 15  
 146 Leu Phe Leu Met Ser Asn Ser Thr Arg Val Phe Lys Thr Asp Ala Gly  
 147 20 25 30  
 149 Glu Met Arg Val Leu Lys Ser His Gly Gly Arg Ile Phe Tyr Arg His  
 150 35 40 45  
 152 Met His Ile Gly Phe Ile Ser Met Glu Pro Lys Ser Leu Phe Val Pro  
 153 50 55 60  
 155 Gln Tyr Leu Asp Ser Asn Leu Ile Ile Phe Ile Arg Arg Gly Glu Ala  
 156 65 70 75 80  
 158 Lys Leu Gly Phe Ile Tyr Asp Asp Glu Leu Ala Glu Arg Arg Leu Lys  
 159 85 90 95  
 161 Thr Gly Asp Leu Tyr Met Ile Pro Ser Gly Ser Ala Phe Tyr Leu Val  
 162 100 105 110  
 164 Asn Ile Gly Glu Gly Gln Arg Leu His Val Ile Cys Ser Ile Asp Pro

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165	115	120	125
167	Ser Thr Ser Leu Gly Leu Glu	Thr Phe Gln Ser Phe Tyr Ile Gly Gly	
168	130	135	140
170	Gly Ala Asn Ser His Ser Val Leu Ser Gly	Phe Glu Pro Ala Ile Leu	
171	145	150	155
173	Glu Thr Ala Phe Asn Glu Ser Arg Thr Val Val Glu Glu Ile Phe Ser		160
174	165	170	175
176	Lys Glu Leu Asp Gly Pro Ile Met Phe Val Asp Asp Ser His Ala Pro		
177	180	185	190
179	Ser Leu Trp Thr Lys Phe Leu Gln Leu Lys Lys Asp Asp Lys Glu Gln		
180	195	200	205
182	Gln Leu Lys Lys Met Met Gln Asp Gln Glu Glu Asp Glu Glu Glu Lys		
183	210	215	220
185	Gln Thr Ser Arg Ser Trp Arg Lys Leu Leu Glu Thr Val Phe Gly Lys		
186	225	230	235
188	Val Asn Glu Lys Ile Glu Asn Lys Asp Thr Ala Gly Ser Pro Ala Ser		240
189	245	250	255
191	Tyr Asn Leu Tyr Asp Asp Lys Lys Ala Asp Phe Lys Asn Ala Tyr Gly		
192	260	265	270
194	Trp Ser Lys Ala Leu His Gly Gly Glu Tyr Pro Pro Leu Ser Glu Pro		
195	275	280	285
197	Asp Ile Gly Val Leu Leu Val Lys Leu Ser Ala Gly Ser Met Leu Ala		
198	290	295	300
200	Pro His Val Asn Pro Ile Ser Asp Glu Tyr Thr Ile Val Leu Ser Gly		
201	305	310	315
203	Tyr Gly Glu Leu His Ile Gly Tyr Pro Asn Gly Ser Lys Ala Met Lys		320
204	325	330	335
206	Thr Lys Ile Lys Gln Gly Asp Val Phe Val Val Pro Arg Tyr Phe Pro		
207	340	345	350
209	Phe Cys Gln Val Ala Ser Arg Asp Gly Pro Leu Glu Phe Phe Gly Phe		
210	355	360	365
212	Ser Thr Ser Ala Arg Lys Asn Lys Pro Gln Phe Leu Ala Gly Ala Ala		
213	370	375	380
215	Ser Leu Leu Arg Thr Leu Met Gly Pro Glu Leu Ser Ala Ala Phe Gly		
216	385	390	395
218	400		400
219	Val Ser Glu Asp Thr Leu Arg Arg Ala Val Asp Ala Gln His Glu Ala		
221	405	410	415
222	420	425	430
224	Leu Lys Met Glu Glu Pro Asn Ala Ile Arg Ser Phe Ala Asn Asp		
225	435	440	445
227	Val Val Met Asp Val Phe		
228	450		
230	<210> SEQ ID NO: 5		
231	<211> LENGTH: 494		
232	<212> TYPE: DNA		
233	<213> ORGANISM: Glycine max		
235	<220> FEATURE:		
236	<221> NAME/KEY: unsure		

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237 <222> LOCATION: (9)  
 238 <223> OTHER INFORMATION: n = A, C, G, or T  
 240 <220> FEATURE:  
 241 <221> NAME/KEY: unsure  
 242 <222> LOCATION: (388)  
 243 <223> OTHER INFORMATION: n = A, C, G, or T  
 245 <220> FEATURE:  
 246 <221> NAME/KEY: unsure  
 247 <222> LOCATION: (392)..(393)  
 248 <223> OTHER INFORMATION: n = A, C, G, or T  
 250 <220> FEATURE:  
 251 <221> NAME/KEY: unsure  
 252 <222> LOCATION: (460)  
 253 <223> OTHER INFORMATION: n = A, C, G, or T  
 255 <220> FEATURE:  
 256 <221> NAME/KEY: unsure  
 257 <222> LOCATION: (463)  
 258 <223> OTHER INFORMATION: n = A, C, G, or T  
 260 <220> FEATURE:  
 261 <221> NAME/KEY: unsure  
 262 <222> LOCATION: (468)  
 263 <223> OTHER INFORMATION: n = A, C, G, or T  
 265 <400> SEQUENCE: 5  
 W--> 266 acacagctng cacatattac atacacgtga atcactaatt aagccatgga gaagaaaatca 60  
 267 atagctgggt tgcgttccct cttccttgtt ctctttgttg ctcaagaagt tgcgtgc 120  
 268 actgaggcaa agacttgcga gaacctggct gatacataca ggggtccatg cttcaccact 180  
 269 ggcagctgcg atgatcactg caagaacaaa gagcacttgc tcagaggcag atgcaggac 240  
 270 gatttcgct gttggtcac caaaaactgt taaatggatc cattcactcc aacgtgaaga 300  
 271 agatgcatgc agcgttattt tataaaaaat acaactacta tatactataat ataataagac 360  
 W--> 272 tgggcgctgc atcaatgacc ctatgtanta tnntatatat tattaccat gtcaagaact 420  
 W--> 273 atagatgcat gtactgtgca taacggctga gttatgtccn tangttanga ataaaaataaa 480  
 274 agtgcgttgc ttgc 494  
 276 <210> SEQ ID NO: 6  
 277 <211> LENGTH: 75  
 278 <212> TYPE: PRT  
 279 <213> ORGANISM: Glycine max  
 281 <400> SEQUENCE: 6  
 282 Met Glu Lys Lys Ser Ile Ala Gly Leu Cys Phe Leu Phe Leu Val Leu  
 283 1 5 10 15  
 285 Phe Val Ala Gln Glu Val Val Val Gln Thr Glu Ala Lys Thr Cys Glu  
 286 20 25 30  
 288 Asn Leu Ala Asp Thr Tyr Arg Gly Pro Cys Phe Thr Thr Gly Ser Cys  
 289 35 40 45  
 291 Asp Asp His Cys Lys Asn Lys Glu His Leu Leu Arg Gly Arg Cys Arg  
 292 50 55 60  
 294 Asp Asp Phe Arg Cys Trp Cys Thr Lys Asn Cys  
 295 65 70 75  
 297 <210> SEQ ID NO: 7  
 298 <211> LENGTH: 30

VERIFICATION SUMMARY  
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L:266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5